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SEQUENCE LISTING

<110> Prayaga, Suhhirdas K
Shimkets, Richard A

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/732,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

<151> 1999-12-10

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 475

<212> DNA

<213> Homo sapiens

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cagcctcttt ttacacaagg gcttgtctga tgcttggaat agggccttcc tggacaaact 180
ccagactgga ttcatcagc agctggaaga cctggagacc tgctttggta tagaggatgg 240
gaagcaagag tctgccttgg aaattgaggg ccctacactg gccataaaga ggtacttcca 300
gggagtacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgtcgt 360
aatggtaaag ggatttttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420
gaactgcaaa aaaaatctgg aaaaggtaat ctatttagca gaagagtgaag agctg 475

<210> 2

<211> 154

<212> PRT

<213> Homo sapiens

<400> 2

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Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His
20 25 30

Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
35 40 45

Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
50 55 60

Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys

20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His
 65 70 75 80
 Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp
 85 90 95
 Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu
 100 105 110
 Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser
 115 120 125
 Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln
 130 135 140
 Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp
 145 150 155 160
 Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln
 165 170 175
 Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys
 180 185 190
 Val Ile Tyr Leu Ala Glu Glu
 195

<210> 5
 <211> 1887
 <212> DNA
 <213> Homo sapiens

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 gcagccgagc tgcggctggc agacaacttc atcgccctccg tgcgccgccg cgacctggcc 240
 aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
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 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggccttggg ccgcctgggc 540
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 cccgacccac tcttctcccc cctgccccctg ctgcgccaggc cccgggggctc gcccgctct 720
 gccctgggtg tggccttttg cggaaccccc ctgcactgca actgcgagct ggtgtggctg 780
 cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt cccacactgc tctggggcggc 840
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cgctcaccac ctctggctgt gcccgaggt cgcccggtg ccctgcgtg ccgggcagt 960
 ggggacccag agccccgtgt gcgttgggtg tcacccagagg gccggctgct aggcaactca 1020
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 agcgtttgct cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccgc 1800
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 cccggccacg aacctgtggg accctag 1887

<210> 6
 <211> 628
 <212> PRT
 <213> Homo sapiens

<400> 6
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 20 25 30
 Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala
 35 40 45
 Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu
 50 55 60
 Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala
 65 70 75 80
 Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg
 85 90 95
 His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu
 100 105 110
 His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg
 115 120 125
 Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala
 130 135 140
 Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp
 145 150 155 160
 Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu
 165 170 175

5
 D
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Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu
 180 185 190
 Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg
 195 200 205
 Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu
 210 215 220
 Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser
 225 230 235 240
 Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu
 245 250 255
 Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys
 260 265 270
 Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu
 275 280 285
 Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro
 290 295 300
 Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val
 305 310 315 320
 Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu
 325 330 335
 Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu
 340 345 350
 Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala
 355 360 365
 Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly
 370 375 380
 Pro Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro
 385 390 395 400
 Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala
 405 410 415
 Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln
 420 425 430
 Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln
 435 440 445
 Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser
 450 455 460
 Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser
 465 470 475 480

Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val
 485 490 495
 Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
 500 505 510
 Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
 515 520 525
 Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
 530 535 540
 Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
 545 550 555 560
 Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
 565 570 575
 Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
 580 585 590
 Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
 595 600 605
 His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
 610 615 620
 Pro Val Gly Pro
 625

<210> 7
 <211> 802
 <212> DNA
 <213> Equus caballus

<400> 7
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 ttttcccat ggccctcctg cctctctct tgcgcccct ggtggtgtac gagttatggc 180
 cctgtggagc tctgggctgt gacctgcctc agaaccacat cctgggttagc aggaagaact 240
 tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaag 300
 acttcagggt cccccaggac atggcgcatg gcaggcagtt cccagaggcc caggccgcgt 360
 ctgtcctcca cgagatgctc cagcagatct tcagcctctt ccacacagag cgctcgtctg 420
 ctgcctggaa cagcaccctc ctggacgaac tctgcacggg actccttcgg cagctggaag 480
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 aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctcttcat 660
 cagcaaacct gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttgaaatg 720
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<210> 8
 <211> 195
 <212> PRT

<213> Homo sapiens

<400> 8

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1 5 10 15
Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30
Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80
His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95
Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110
His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140
Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160
Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175
Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190
Gly Ser Ser
195

<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
1 5 10 15
Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu
20 25 30
Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu
 50 55 60
 Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu
 65 70 75 80
 Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser
 85 90 95
 Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu
 100 105 110
 His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly
 115 120 125
 Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys
 130 135 140
 Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser
 145 150 155 160
 Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser
 165 170 175
 Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu
 180 185 190
 Gly Ser Pro
 195

<210> 10
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:pfam00143
 Domain 71-187

<400> 10
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 Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn
 20 25 30
 Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr
 35 40 45
 Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro
 50 55 60
 Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr
 65 70 75 80

Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys
85 90 95

Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser
100 105 110

Ser Thr Ala Leu Gln
115

<210> 11

<211> 194

<212> PRT

<213> Felis catus

<400> 11

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val
115 120 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser
180 185 190

Glu Lys

<210> 12

<211> 195
 <212> PRT
 <213> Homo sapiens

<400> 12

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
 1 5 10 15

Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu
 20 25 30

Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser
 35 40 45

Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu
 50 55 60

Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu
 65 70 75 80

His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser
 85 90 95

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu
 100 105 110

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly
 115 120 125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys
 130 135 140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser
 145 150 155 160

Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser
 165 170 175

Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu
 180 185 190

Ser Ser Pro
 195

D5
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<210> 13
 <211> 195
 <212> PRT
 <213> Equus caballus

<400> 13

Met Ala Leu Leu Pro Ser Leu Leu Thr Ala Leu Val Val Tyr Glu Leu
 1 5 10 15

Trp Pro Cys Gly Ala Leu Gly Cys Asp Leu Pro Gln Asn His Ile Leu
 20 25 30

Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser
 35 40 45
 Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp
 50 55 60
 Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu
 65 70 75 80
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95
 Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu
 100 105 110
 Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly
 115 120 125
 Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys
 130 135 140
 Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser
 145 150 155 160
 Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser
 165 170 175
 Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu
 180 185 190
 Gly Ser Pro
 195

<210> 14
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
 1 5 10 15
 Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
 20 25 30
 Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
 35 40 45
 Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
 50 55 60
 Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
 65 70 75 80
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
 85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

<210> 15
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Consensus
sequence

<400> 15
Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser
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Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu
50 55 60

Gln
65

<210> 16
<211> 166
<212> PRT
<213> Homo sapiens

<400> 16
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
 20 25 30
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35 40 45
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
 100 105 110
 Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 115 120 125
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 130 135 140
 Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
 145 150 155 160
 Thr Gly Tyr Leu Arg Asn
 165

<210> 17
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 17
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
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 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20 25 30
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35 40 45
 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50 55 60
 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65 70 75 80
 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85 90 95
 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn

100	105	110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu		
115	120	125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg		
130	135	140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser		
145	150	155
160		
Leu Arg Ser Lys Glu		
165		

<210> 18
 <211> 189
 <212> PRT
 <213> Mus musculus

18		
Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr		
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15		
Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu		
20	25	30
Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser		
35	40	45
Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu		
50	55	60
Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu		
65	70	75
80		
Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser		
85	90	95
Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu		
100	105	110
His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly		
115	120	125
Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg		
130	135	140
Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser		
145	150	155
160		
Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser		
165	170	175
Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys		
180	185	

D5
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<210> 19
 <211> 195
 <212> PRT
 <213> Antilocapra americana

<400> 19
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 Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro
 20 25 30
 Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser
 35 40 45
 Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu
 50 55 60
 Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu
 65 70 75 80
 His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser
 85 90 95
 Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu
 100 105 110
 His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly
 115 120 125
 Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys
 130 135 140
 Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser
 145 150 155 160
 Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser
 165 170 175
 Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu
 180 185 190
 Ala Ser Ser
 195

<210> 20
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Consensus
 sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
 1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
 20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
 35 40

<210> 21

<211> 184

<212> PRT

<213> Equus caballus

<400> 21

Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys
 1 5 10 15

His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu
 20 25 30

Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser
 35 40 45

Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu
 50 55 60

Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val
 65 70 75 80

His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser
 85 90 95

Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu
 100 105 110

Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly
 115 120 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg
 130 135 140

Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
 145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser
 165 170 175

Ser Ser Thr Asn Leu Pro Gln Ser
 180

<210> 22

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus
sequence

<400> 22

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
85 90

<210> 23

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 23

gcctggctcc ctctcgctga gacacacata cactcacaca tacacaaccc ggcaggctcg 60
tctgaacttg aagacacccc acattccaag atgcccaggg ttcttgggaa tgcctgggggt 120
tcttcgatcc ggaaaatcct accggcatcc tcttagggag ggattattat tattattttt 180
ctttaatctg gaagagaaga gaacaagttg tgcttttccc cccttcttct tgctaaacgc 240
catggatata actgaataag cggctcaggg ctttccccgc gtggacgtcc gaggccacca 300
tctgcctgca ttcgccggag ccgccggagg gtttagctcg agtctgtctc gggcggggaa 360
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gccgggggta gatgctgctt cgcccaggcg ctgagtgacc agaccatgga gacctgctt 480
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gtacccctg atattgaccg gcggacagtg gagctgcgcc tgggcggcaa cttcatcatc 660
cacatcagcc gccaggactt tgccaacatg acggggctgg tggacctgac cctgtccagg 720
aacaccatca gccacatcca gcccttttcc tttctggacc tcgagagcct ccgctccctg 780
catcttgaca gcaatcgggt gccaaagcctt ggggaggaca ccctccgggg cctggtcaac 840
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gacttcctgc tgacattgga ggatctggac ctctcctaca acaacctcca tggcctgccg 960
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gatgaccgcc tggtagggaa ctctcaagg accgctgtct atgacaatgg caccctggac 1500
atcttcatca ccacatctca ggacagtggg gccttcacct gcattgctgc caatgctgcc 1560
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 aacatcgtgg gctgcgcccc gttcttcacc aaggctgact acccgagtg ccagtccatg 2040
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 cctccccacc acccgccgg ggtgtgctca gggaatgtgg actcgtcaa atgccggact 3060
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 gcaagcggct ttggattgct tatg 3144

<210> 24
 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 24
 Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser
 1 5 10 15
 Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg
 20 25 30
 Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu
 35 40 45
 Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys
 50 55 60
 Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu
 65 70 75 80
 Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg
 85 90 95
 Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg
 100 105 110
 Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg
 115 120 125

Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser
 130 135 140
 Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu
 145 150 155 160
 Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn
 165 170 175
 Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu
 180 185 190
 Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro
 195 200 205
 Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp
 210 215 220
 His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln
 225 230 235 240
 Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro
 245 250 255
 Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr
 260 265 270
 Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His
 275 280 285
 Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp
 290 295 300
 Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp
 305 310 315 320
 His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln
 325 330 335
 His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys
 340 345 350
 Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro
 355 360 365
 Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn
 370 375 380
 Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe
 385 390 395 400
 Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu
 405 410 415
 Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr
 420 425 430

Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr
 435 440 445
 Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser Pro
 450 455 460
 Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala Leu
 465 470 475 480
 Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln
 485 490 495
 Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile
 500 505 510
 Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr
 515 520 525
 Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr
 530 535 540
 Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala
 545 550 555 560
 Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr
 565 570 575
 Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe
 580 585 590
 Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro
 595 600 605
 Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly
 610 615 620
 Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln
 625 630 635 640
 Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala
 645 650 655
 Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly Ser
 660 665 670
 Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser
 675 680 685
 Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala
 690 695 700
 Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg
 705 710 715 720
 Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser
 725 730 735

D5
 Cont

Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu
 740 745 750
 Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp
 755 760 765
 Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly
 770 775 780
 Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu
 785 790 795 800
 Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly
 805 810 815
 Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val
 820 825 830

<210> 25
 <211> 98
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:IFAbd Domain
 13-110

<400> 25
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 1 5 10 15
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 20 25 30
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 35 40 45
 His Leu Lys Thr Val Leu Glu Lys Leu Glu Lys Glu Asp Phe Thr
 50 55 60
 Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 65 70 75 80
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 85 90 95
 Ile Val

<210> 26
 <211> 183

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143

Domain 5-187

<400> 26

Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg
20 25 30

Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys
35 40 45

Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly
50 55 60

Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn
65 70 75 80

Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala
85 90 95

Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln
100 105 110

Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu
115 120 125

Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg
130 135 140

Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr
165 170 175

Tyr Ser Ser Thr Ala Leu Gln
180

<210> 27

<211> 786

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Thr Leu Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala
1 5 10 15

Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu
20 25 30

Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro
 35 40 45
 Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile
 50 55 60
 Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp
 65 70 75 80
 Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe
 85 90 95
 Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu
 100 105 110
 Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His
 115 120 125
 Leu Ile Val Asn Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe
 130 135 140
 Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn
 145 150 155 160
 Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His
 165 170 175
 Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr
 180 185 190
 Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg
 195 200 205
 Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser
 210 215 220
 Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly
 225 230 235 240
 Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu
 245 250 255
 Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys
 260 265 270
 Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro
 275 280 285
 Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln
 290 295 300
 Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile
 305 310 315 320
 His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr
 325 330 335

Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln
 340 345 350
 Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala
 355 360 365
 Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn
 370 375 380
 Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr
 385 390 395 400
 Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu
 405 410 415
 Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr
 420 425 430
 Thr Thr Ser Ala Leu Val Lys Trp Ser Ser Val Ser Lys Ser Ala Pro
 435 440 445
 Arg Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Glu Val Leu
 450 455 460
 Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn
 465 470 475 480
 Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp
 485 490 495
 Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln
 500 505 510
 Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln
 515 520 525
 Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Val Ala Thr
 530 535 540
 Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn
 545 550 555 560
 His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser
 565 570 575
 Gln Thr Asn Gly Ala Gln Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala
 580 585 590
 Pro Pro Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp
 595 600 605
 Phe Thr Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser
 610 615 620
 Leu Gly Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Trp Arg Ile Pro
 625 630 635 640

D5
 cont

Pro Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala
645 650 655

Phe Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp
660 665 670

Ser Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His
675 680 685

His Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg
690 695 700

Ser Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser
705 710 715 720

Phe Asp Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro
725 730 735

Gly Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg
740 745 750

Ser Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu
755 760 765

Val Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser
770 775 780

Thr Val
785